1. A method of determining the extent of somatic genomic damage of tumor cells from an individual patient with colorectal cancer, which genomic damage fraction is useful as a prognostic indicator of clinical outcome of said cancer patient, comprising

   a. amplifying by AP-PCR DNA fingerprinting DNA fragments from the tumor and normal tissue cells from the same individual patient;

   b. determining the number of fingerprint bands with altered intensities from step (a) according to predetermined criteria between the tumor and normal tissues of said subject;

   c. determining the Genomic Damage Fraction (GDF) from the results of steps (a) and (b) by dividing the number of altered AP-PCR fingerprint bands by the total number of bands of said subject;

   d. determining the prognosis of said subject according to said subject's GDF, where a GDF greater than a predetermined GDF is indicative of a poor clinical outcome, and a GDF lesser than a predetermined GDF is indicative of a better clinical outcome.

2. The method of claim 1, wherein said altered intensity of the AP-PCR fingerprint bands is a decreased intensity in tumor DNA relative to normal tissue DNA from said individual colorectal cancer patient that is a reflection of the presence of less than the normal number of copies of chromosomal sequences surrounding the fingerprint band in the tumor cell genome (i.e. genomic sequence loss).

3. The method of claim 1, wherein said altered intensity of the AP-PCR fingerprint bands is an increased intensity in tumor DNA relative to normal tissue DNA from said individual colorectal cancer patient that is a reflection of the presence of more than the normal number of copies of chromosomal sequences surrounding the fingerprint band in the tumor cell genome (i.e. genomic sequence gain).

4. The method of claim 1 wherein the GDF is obtained by scoring the genomic sequence losses from claim 2.

5. The method of claim 1 wherein the GDF is obtained by scoring the genomic sequence gains from claim 3.

6. The method of claim 1 wherein the GDF is obtained by scoring both genomic sequence losses and gains from claims 2 and 3.

7. The method of claim 1, wherein said GDF is obtained by the combined AP-PCR DNA fingerprint bands generated by AP-PCR DNA fingerprinting with arbitrary primers MCG1 (SEQ ID No: 1) and BLUE (SEQ ID No: 2).

8. The method of claim 1, wherein said poor clinical outcome is death from recurrent colorectal cancer.

9. The method of claim 1, wherein said better clinical outcome is absence of death from recurrent colorectal cancer.

10. The method of claim 1, wherein said subject is a patient of gastrointestinal cancer.

11. The method of claim 1, wherein said subject is a patient of any cancer.

12. A method of determining somatic genomic alterations of tumor cells from individual patients with colorectal cancer, which genomic alterations are useful as a prognostic indicators of clinical outcome of said cancer patients, comprising

    a. amplifying by AP-PCR DNA fingerprinting DNA fragments from the genome of tumor and normal tissue cells from the same individual patients;

    b. determining the relative frequency of genomic alterations by scoring fingerprint bands with altered intensities from step (a) between the tumor and normal tissues of said subjects;

    c. determining the prognostic value of any altered bands from step (b) by searching for statistical correlation of said alterations with the previously known clinical outcome of a group of colorectal cancer patients;

    d. determining the prognosis of an individual colorectal cancer patient according to said patient's status for the bands with prognostic value of step (c), where the presence of alteration of said band is indicative of a poor clinical outcome, and the absence of alteration of said band is indicative of a better clinical outcome.

13. The method of claim 12, wherein said somatic genomic alteration is as in claims 2 or 3.

14. The method of claim 12, wherein said somatic genomic alteration is a particular combination of the type of alterations of claims 2 and 3.

15. The method of claim 12, wherein said useful genomic alterations are obtained by AP-PCR DNA fingerprinting with arbitrary primers MCG1 (SEQ ID No: 1) and BLUE (SEQ ID No: 2).

16. The method of claim 12, wherein said poor clinical outcome is death from recurrent colorectal cancer.

17. The method of claim 12, wherein said poor clinical outcome is absence of death from recurrent colorectal cancer.

18. The method of claim 12, wherein said subject is a patient of gastrointestinal cancer.

19. The method of claim 12, wherein said subject is a patient of any cancer.

20. A method of determining somatic genomic alterations at certain chromosomal regions of tumor cells from individual patients with colorectal cancer, which genomic alterations are useful as a prognostic indicators of clinical outcome of said cancer patients, comprising

    a. generating AP-PCR fingerprints from tumor and normal tissue cells from the same individual patients for which the chromosomal localization of the fingerprint DNA fragments has been previously determined;

    b. determining the relative frequency of genomic alterations by scoring fingerprint bands with altered intensities from step (a) between the tumor and normal tissues of said subjects,

thus generating an amplotype of said colorectal cancer;

c. identifying chromosomal regions from AP-PCR fingerprinting data of steps (a) and (b) wherein the occurrence of gains or losses of genomic sequences are prognostic of the clinical outcome of said cancer patients as determined in claim 12.

21. The method of claim 20, wherein said amplotype of colorectal cancer is obtained by AP-PCR DNA fingerprinting with arbitrary primers MCG1 (SEQ ID No: 1) and BLUE (SEQ ID No: 2).

22. A method of determining somatic genomic alterations of tumor cells from individual patients with colorectal cancer, which genomic alterations are useful as a prognostic indicators of clinical outcome of said cancer patients, comprising

a. generating the AP-PCR DNA fingerprint of non-cancerous cells from said patient;

b. generating the AP-PCR DNA fingerprint of primary cancer cells from said patient;

c. generating the AP-PCR DNA fingerprint of metastatic cancer cells from said patient;

d. identifying chromosomal regions from AP-PCR DNA fingerprint data of steps (a), (b) and (c) wherein the occurrence of gains or losses of genomic sequences are prognostic of the clinical outcome of said cancer patients as determined in claim 12.

23. The method of claim 22, wherein the gain and loss of nucleic acids is significantly different in metastatic cancer cells as compared to primary cancer cells.

24. The method of claim 22, wherein said chromosomal region is determined by a band of chromosome 4 obtained using the Blue primer.

25. The method of claim 22, wherein said band is band N from the DNA fingerprint generated with the Blue primer (SEQ ID. 3).

26. A method of identifying a genomic region relevant for prognosis of a cancer in a subject having said cancer comprising,

a. generating the AP-PCR DNA fingerprint of non-cancerous cells, primary cancer, and metastatic tumor cells from said subject; and

b. identifying said genomic regions from AP-PCR DNA fingerprint data of step (a), showing gains and losses of genomic sequences from certain genomic regions thereby identifying a genomic region linked to a cancer gene; and

c. identifying genomic sequences within the chromosomal region of step (b) that can be utilized for estimation of the alteration (gains and losses) in this genomic region that are useful for predicting clinical outcome of said colorectal cancer patient.

27. The method of claims 20, 22 and 26, wherein said cancer is any gastrointestinal cancer.

28. The method of claims 20, 22 and 26, wherein said cancer is any cancer.